



#4A

1

SEQUENCE LISTING

<110> Rosanne M. Crooke
Mark J. Graham
Kristina M. Lemonidis

<120> ANTISENSE MODULATION OF ACYL COA CHOLESTEROL ACYLTRANSFERASE-2
EXPRESSION

<130> ISPH-0588

<140> US/09/918,026

<141> 2001-07-30

<160> 65

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<212> DNA

<213> Artificial Sequence

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<223> Antisense Oligonucleotide

<400> 1

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<223> Antisense Oligonucleotide

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atgcattctg cccccaagga

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<210> 3

<211> 1569

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1569)

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Met Glu Pro Gly Gly Ala Arg Leu Arg Leu Gln Arg Thr Glu Gly Leu

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5

10

15

gga ggg gag cgg gag cgc caa ccc tgt gga gat gga aac act gag acg 96

Gly Gly Glu Arg Glu Arg Gln Pro Cys Gly Asp Gly Asn Thr Glu Thr

20

25

30

cac aga gcc ccg gac ttg gta caa tgg acc cga cac atg gag gct gtg 144

His	Arg	Ala	Pro	Asp	Leu	Val	Gln	Trp	Thr	Arg	His	Met	Glu	Ala	Val		
		35					40					45					
aag	gca	caa	ttg	ctg	gag	caa	gcg	cag	gga	caa	ctg	agg	gag	ctg	ctg	192	
Lys	Ala	Gln	Leu	Leu	Glu	Gln	Ala	Gln	Gly	Gln	Leu	Arg	Glu	Leu	Leu		
	50					55					60						
gat	cgg	gcc	atg	cgg	gag	gct	ata	caa	tcc	tac	cca	tca	caa	gac	aaa	240	
Asp	Arg	Ala	Met	Arg	Glu	Ala	Ile	Gln	Ser	Tyr	Pro	Ser	Gln	Asp	Lys		
65					70				75						80		
cct	ctg	ccc	cca	cct	ccc	cca	ggg	tcc	ttg	agc	agg	acc	cag	gag	cca	288	
Pro	Leu	Pro	Pro	Pro	Pro	Pro	Gly	Ser	Leu	Ser	Arg	Thr	Gln	Glu	Pro		
				85					90					95			
tcc	ctg	ggg	aaa	cag	aaa	gtt	ttc	atc	atc	cgc	aag	tcc	ctg	ctt	gat	336	
Ser	Leu	Gly	Lys	Gln	Lys	Val	Phe	Ile	Ile	Arg	Lys	Ser	Leu	Leu	Asp		
			100					105					110				
gag	ctg	atg	gag	gtg	cag	cat	ttc	cgc	acc	atc	tac	cac	atg	ttc	atc	384	
Glu	Leu	Met	Glu	Val	Gln	His	Phe	Arg	Thr	Ile	Tyr	His	Met	Phe	Ile		
		115					120					125					
gct	ggc	ctg	tgt	gtc	ttc	atc	atc	agc	acc	ctg	gcc	atc	gac	ttc	att	432	
Ala	Gly	Leu	Cys	Val	Phe	Ile	Ile	Ser	Thr	Leu	Ala	Ile	Asp	Phe	Ile		
	130					135					140						
gat	gag	ggc	agg	ctg	ctg	ctg	gag	ttt	gac	cta	ctg	atc	ttc	agc	ttc	480	
Asp	Glu	Gly	Arg	Leu	Leu	Leu	Glu	Phe	Asp	Leu	Leu	Ile	Phe	Ser	Phe		
145					150				155						160		
gga	cag	ctg	cca	ttg	gcg	ctg	gtg	acc	tgg	gtg	ccc	atg	ttt	ctg	tcc	528	
Gly	Gln	Leu	Pro	Leu	Ala	Leu	Val	Thr	Trp	Val	Pro	Met	Phe	Leu	Ser		
				165					170					175			
acc	ctg	ttg	gcg	ccg	tac	cag	gcc	cta	cgg	ctg	tgg	gcc	agg	ggc	acc	576	
Thr	Leu	Leu	Ala	Pro	Tyr	Gln	Ala	Leu	Arg	Leu	Trp	Ala	Arg	Gly	Thr		
			180					185					190				
tgg	acg	cag	gcg	acg	ggc	ctg	ggc	tgt	gcg	ctt	tta	gcc	gcc	cac	gcc	624	
Trp	Thr	Gln	Ala	Thr	Gly	Leu	Gly	Cys	Ala	Leu	Leu	Ala	Ala	His	Ala		
		195					200					205					
gtg	gtg	ctc	tgc	gcg	ctg	ccg	gtc	cac	gtg	gcc	gtg	gag	cat	cag	ctc	672	
Val	Val	Leu	Cys	Ala	Leu	Pro	Val	His	Val	Ala	Val	Glu	His	Gln	Leu		
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ccg	ccg	gcc	tcc	cgt	tgt	gtc	ctg	gtc	ttc	gag	cag	gtt	agg	ttc	ctg	720	
Pro	Pro	Ala	Ser	Arg	Cys	Val	Leu	Val	Phe	Glu	Gln	Val	Arg	Phe	Leu		
225					230					235					240		
atg	aaa	agc	tac	tcc	ttc	ctg	aga	gag	gct	gtg	cct	ggg	atc	ctt	cgt	768	
Met	Lys	Ser	Tyr	Ser	Phe	Leu	Arg	Glu	Ala	Val	Pro	Gly	Ile	Leu	Arg		
				245					250					255			
gcc	aga	cga	ggg	gag	ggg	atc	cag	gcc	ccc	agt	ttc	tcc	agc	tac	ctc	816	
Ala	Arg	Arg	Gly	Glu	Gly	Ile	Gln	Ala	Pro	Ser	Phe	Ser	Ser	Tyr	Leu		
			260					265					270				

tac ttc ctc ttc tgc cca aca ctc atc tac agg gag act tac cct agg	864
Tyr Phe Leu Phe Cys Pro Thr Leu Ile Tyr Arg Glu Thr Tyr Pro Arg	
275 280 285	
acg ccc tat gtc agg tgg aat tat gtg gcc aag aac ttt gcc cag gcc	912
Thr Pro Tyr Val Arg Trp Asn Tyr Val Ala Lys Asn Phe Ala Gln Ala	
290 295 300	
ctg gga tgt gtg ctc tat gcc tgc ttc atc ctg ggc cgc ctc tgt gtt	960
Leu Gly Cys Val Leu Tyr Ala Cys Phe Ile Leu Gly Arg Leu Cys Val	
305 310 315 320	
cct gtc ttt gcc aac atg agc cga gag ccc ttc agc acc cgt gcc ctg	1008
Pro Val Phe Ala Asn Met Ser Arg Glu Pro Phe Ser Thr Arg Ala Leu	
325 330 335	
gtg ctc tct atc ctg cat gcc acg ttg cca ggc atc ttc atg ctg ctg	1056
Val Leu Ser Ile Leu His Ala Thr Leu Pro Gly Ile Phe Met Leu Leu	
340 345 350	
ctc atc ttc ttt gcc ttc ctc cat tgc tgg ctc aac gcc ttt gcc gag	1104
Leu Ile Phe Phe Ala Phe Leu His Cys Trp Leu Asn Ala Phe Ala Glu	
355 360 365	
atg cta cga ttt gga gac agg atg ttc tac cgg gac tgg tgg aac tca	1152
Met Leu Arg Phe Gly Asp Arg Met Phe Tyr Arg Asp Trp Trp Asn Ser	
370 375 380	
acg tcc ttc tcc aac tac tac cgc act tgg aac gtg gtg gtc cat gac	1200
Thr Ser Phe Ser Asn Tyr Tyr Arg Thr Trp Asn Val Val Val His Asp	
385 390 395 400	
tgg ctg tac agc tac gtg tat cag gat ggg ctg cgg ctc ctt ggt gcc	1248
Trp Leu Tyr Ser Tyr Val Tyr Gln Asp Gly Leu Arg Leu Leu Gly Ala	
405 410 415	
cgg gcc cga ggg gta gcc atg ctg ggt gtg ttc ctg gtc tcc gca gtg	1296
Arg Ala Arg Gly Val Ala Met Leu Gly Val Phe Leu Val Ser Ala Val	
420 425 430	
gcc cat gag tat atc ttc tgc ttc gtc ctg ggg ttc ttc tat ccc gtc	1344
Ala His Glu Tyr Ile Phe Cys Phe Val Leu Gly Phe Phe Tyr Pro Val	
435 440 445	
atg ctg ata ctc ttc ctt gtc att gga gga atg ttg aac ttc atg atg	1392
Met Leu Ile Leu Phe Leu Val Ile Gly Gly Met Leu Asn Phe Met Met	
450 455 460	
cat gac cag cgc acc ggc ccg gca tgg aac gtg ctg atg tgg acc atg	1440
His Asp Gln Arg Thr Gly Pro Ala Trp Asn Val Leu Met Trp Thr Met	
465 470 475 480	
ctg ttt cta ggc cag gga atc cag gtc agc ctg tac tgc cag gag tgg	1488
Leu Phe Leu Gly Gln Gly Ile Gln Val Ser Leu Tyr Cys Gln Glu Trp	
485 490 495	
tac gca cgg cgg cac tgc ccc tta ccc cag gca act ttc tgg ggg ctg	1536
Tyr Ala Arg Arg His Cys Pro Leu Pro Gln Ala Thr Phe Trp Gly Leu	
500 505 510	

gtg aca cct cga tct tgg tcc tgc cat acc tag
 Val Thr Pro Arg Ser Trp Ser Cys His Thr *
 515 520

1569

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 cccgggcacc aagga

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<210> 6
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<220>
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 ctacgtgtat caggatgggc tgcgg

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<400> 7
 gaaggtgaag gtcggagtc

19

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<400> 8

gaagatggtg atgggatttc

20

<210> 9

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<400> 9

caagcttccc gttctcagcc

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<213> Mus musculus

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<222> (30)...(1607)

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<221> unsure

<222> (176)

<223> a, c, g or t

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			1				5				

cgg	agg	aga	gaa	ggg	ctg	gga	gag	gag	cag	gag	aag	gga	gcc	cgt	gga	101
Arg	Arg	Arg	Glu	Gly	Leu	Gly	Glu	Glu	Gln	Glu	Lys	Gly	Ala	Arg	Gly	
10					15						20					

gga	gaa	ggg	aac	gca	agg	aca	cac	gga	acc	cca	gac	ttg	gtg	caa	tgg	149
Gly	Glu	Gly	Asn	Ala	Arg	Thr	His	Gly	Thr	Pro	Asp	Leu	Val	Gln	Trp	
25				30					35						40	

act	cga	cat	atg	gag	gct	gtg	aag	acn	cag	ttt	ctg	gag	caa	gca	cag	197
Thr	Arg	His	Met	Glu	Ala	Val	Lys	Thr	Gln	Phe	Leu	Glu	Gln	Ala	Gln	
			45					50						55		

aga	gag	ttg	gca	gag	ctg	ttg	gat	cgg	gcc	cta	tgg	gag	gct	atg	caa	245
Arg	Glu	Leu	Ala	Glu	Leu	Leu	Asp	Arg	Ala	Leu	Trp	Glu	Ala	Met	Gln	
			60					65						70		

gct	tac	ccc	aaa	caa	gac	aga	cct	ctt	ccc	tcc	gct	gcc	cca	gat	tct	293
Ala	Tyr	Pro	Lys	Gln	Asp	Arg	Pro	Leu	Pro	Ser	Ala	Ala	Pro	Asp	Ser	
		75					80					85				

aca	agc	aag	acc	ccg	gag	tta	cgc	cct	gga	aaa	cgg	aaa	gtt	ttc	gtc	341
Thr	Ser	Lys	Thr	Pro	Glu	Leu	Arg	Pro	Gly	Lys	Arg	Lys	Val	Phe	Val	
	90					95					100					

gcc	cgc	aag	tca	ctg	atc	gat	gag	cta	atg	gag	gtg	caa	cat	ttc	cga	389
Ala	Arg	Lys	Ser	Leu	Ile	Asp	Glu	Leu	Met	Glu	Val	Gln	His	Phe	Arg	
105					110					115					120	

acc atc tac cac atg ttc ata gcg ggc cta tgg ttc ttg atc atc agc	437
Thr Ile Tyr His Met Phe Ile Ala Gly Leu Trp Phe Leu Ile Ile Ser	
125 130 135	
acc ctg gcc atc gac ttc att gat gag ggc agg ttg atg ctg gag ttt	485
Thr Leu Ala Ile Asp Phe Ile Asp Glu Gly Arg Leu Met Leu Glu Phe	
140 145 150	
gac tta ctc ctc ttc agc ttc gga cag ctg ccc ttg gcg ctg atg acc	533
Asp Leu Leu Leu Phe Ser Phe Gly Gln Leu Pro Leu Ala Leu Met Thr	
155 160 165	
tgg gtt ccc atg ttc ctg tat acg ctc cta gtg ccc tac cag acc ctg	581
Trp Val Pro Met Phe Leu Tyr Thr Leu Leu Val Pro Tyr Gln Thr Leu	
170 175 180	
tgg ctg tgg gcc agg ccg cgc gct ggg ggt gcc tgg atg ctg ggg gcc	629
Trp Leu Trp Ala Arg Pro Arg Ala Gly Gly Ala Trp Met Leu Gly Ala	
185 190 195 200	
agc ctg ggc tgc gtt ctg ctg gct gcc cac gct gtg gtg ctc tgc gtc	677
Ser Leu Gly Cys Val Leu Leu Ala Ala His Ala Val Val Leu Cys Val	
205 210 215	
ctg ccg gtg cac gtg tca gtg agg cat gag ctt ccg ccc gcc tcg cgc	725
Leu Pro Val His Val Ser Val Arg His Glu Leu Pro Pro Ala Ser Arg	
220 225 230	
tgc gtg ctg gtc ttt gag cag gtc aga ttg ctg atg aaa agc tac tcc	773
Cys Val Leu Val Phe Glu Gln Val Arg Leu Leu Met Lys Ser Tyr Ser	
235 240 245	
ttc ctg aga gag act gtg cct ggg atc ttt tgt gtc aga cga gga aag	821
Phe Leu Arg Glu Thr Val Pro Gly Ile Phe Cys Val Arg Arg Gly Lys	
250 255 260	
ggc atc agc ccc cca agt ttc tcc agc tac ctc tac ttc ctc ttc tgc	869
Gly Ile Ser Pro Pro Ser Phe Ser Ser Tyr Leu Tyr Phe Leu Phe Cys	
265 270 275 280	
cct aca ctt atc tac aga gag aca tac ccc agg aca ccc agc atc agg	917
Pro Thr Leu Ile Tyr Arg Glu Thr Tyr Pro Arg Thr Pro Ser Ile Arg	
285 290 295	
tgg aac tat gtg gcc aag aac ttt gcc cag gtc ctg ggc tgt ttg ctc	965
Trp Asn Tyr Val Ala Lys Asn Phe Ala Gln Val Leu Gly Cys Leu Leu	
300 305 310	
tat gcc tgc ttc atc ctg ggc cgc ctc tgt gtc cct gtc ttt gcc aac	1013
Tyr Ala Cys Phe Ile Leu Gly Arg Leu Cys Val Pro Val Phe Ala Asn	
315 320 325	
atg agc cgg gaa ccc ttc agc acc cgg gct ctg ctg ctc tcc atc ttg	1061
Met Ser Arg Glu Pro Phe Ser Thr Arg Ala Leu Leu Ser Ile Leu	
330 335 340	
cat gcc acg ggg cca ggc atc ttc atg ctg ctc ctc atc ttc ttc gcc	1109
His Ala Thr Gly Pro Gly Ile Phe Met Leu Leu Leu Ile Phe Phe Ala	

345	350	355	360	
ttc ctg cac tgc tgg ctc aac gcc ttc gcc gag atg ctg cgg ttt gga				1157
Phe Leu His Cys Trp Leu Asn Ala Phe Ala Glu Met Leu Arg Phe Gly	365	370	375	
gac agg atg ttc tac cgg gac tgg tgg aac tcg act tcc ttc tcc aac				1205
Asp Arg Met Phe Tyr Arg Asp Trp Trp Asn Ser Thr Ser Phe Ser Asn	380	385	390	
tac tac cgc acc tgg aac gtc gtg gtc cat gac tgg ctg tac agc tat				1253
Tyr Tyr Arg Thr Trp Asn Val Val Val His Asp Trp Leu Tyr Ser Tyr	395	400	405	
gtg tat caa gat ggg ctg tgg ctc tta ggc agg cgg gct cgc ggg gtg				1301
Val Tyr Gln Asp Gly Leu Trp Leu Leu Gly Arg Arg Ala Arg Gly Val	410	415	420	
gcc atg ctg gga gtg ttc ctg gtg tct gcg gtg gtt cat gag tat atc				1349
Ala Met Leu Gly Val Phe Leu Val Ser Ala Val Val His Glu Tyr Ile	425	430	435	440
ttc tgc ttc gtc ctg ggg ttc ttc tac ccg gtc atg ctg atg cta ttc				1397
Phe Cys Phe Val Leu Gly Phe Phe Tyr Pro Val Met Leu Met Leu Phe	445	450	455	
ctt gtt ttc ggg ggg ctg ctg aat ttc acc atg aac gac agg cac aca				1445
Leu Val Phe Gly Gly Leu Leu Asn Phe Thr Met Asn Asp Arg His Thr	460	465	470	
ggt cca gcc tgg aac atc ctg atg tgg acc ttt ctc ttc atg ggc cag				1493
Gly Pro Ala Trp Asn Ile Leu Met Trp Thr Phe Leu Phe Met Gly Gln	475	480	485	
ggc atc cag gtc agc cta tac tgc cag gag tgg tat gct cgt cga cac				1541
Gly Ile Gln Val Ser Leu Tyr Cys Gln Glu Trp Tyr Ala Arg Arg His	490	495	500	
tgt ccc ctg ccc cag aca aca ttc tgg ggg atg gtg aca ccc caa tct				1589
Cys Pro Leu Pro Gln Thr Thr Phe Trp Gly Met Val Thr Pro Gln Ser	505	510	515	520
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Trp Ser Cys His Thr *	525			

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<400> 11

gggagcccgt ggagga

16

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 aaggggaacgc aaggacacac ggaa 24

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<400> 34

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<210> 37

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<210> 45

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<400> 46

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<210> 47

<211> 20

<212> DNA

<213> Artificial Sequence

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